

SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

<140> 09/256,000

<141> 1999-02-23

<150> 60/075,508

<151> 1998-02-23

<160> 26

<170> PatentIn Ver. 2.0

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<211> 1548

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (26)..(1423)

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aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta	100
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu	
10 15 20 25	

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc	148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
30 35 40	

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
45 50 55	

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	
60 65 70	

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc	292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Leu Ala Ala Arg Ser	
75 80 85	

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag	340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
90 95 100 105	

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc	388
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330	335	340	345	
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser				1108
350 355 360				
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg				1156
365 370 375				
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val				1204
380 385 390				
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu				1252
395 400 405				
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu				1300
410 415 420 425				
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp				1348
430 435 440				
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp				1396
445 450 455				
tgtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc gggggcgctg Val Lys Asn Ser Glu Gly Asp Cys Ala				1443
460 465				
Ggctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg aagagctgcc				1503
Gctggcacct ggcaccacaa gaccatgttt tctaagaacc atttt				1548
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<213> Homo sapiens				
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Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln				
20 25 30				
Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala				
35 40 45				
Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu				
50 55 60				

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
65 70 75 80

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
 370 375 380
 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
 385 390 395 400
 Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
 405 410 415
 Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
 420 425 430
 Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
 435 440 445
 Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
 450 455 460
 Cys Ala
 465

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<210> 3
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 130, 186, and 205 are
      either A, T, G, or C.

<400> 3
agcgaccgtg agaagtca gaggccttcct gtggAACCGT tcatggaccc agacaaAGTG 60
accaggCCA cagcccAGAT tgggttcatc aagtTTGCCG tgatCCCAat gtttGAAACA 120
gtgaccaAGN tcttccccat ggTTGAGGAG atcatgCTGC agccACTTTG ggaatCCCGA 180
gatcgntACG aggAGCTGAA gcggntAGAT gacGCCATGA aAGAG 225
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<210> 4
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 12, 36, 61, and 109 are
      either A, T, G, or C.

<400> 4
gtaccagatc antgccccgca cagagctggc ggtccgntac aatgacatct caccgttgg 60
gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120
ccaacatccc acctgatggg ttcaaggaga tccgacag 158
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<210> 5
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 14, 22, and 50 are either A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaaggcaga tccgacag 98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411 are either A, T, G, or C.

<400> 6
nggttaactg ggcgcatttg tctttctctg agaacagcga tctggttatg gggcatttct 60
gtctctaactg tcactgtctg ctgcattccc tgcaagcga ccgtgagaag tcagaaggcc 120
ttccctgtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tccccatggg 240
tgagggaga ttcatgctgg cagccanttt gggaatccc gaggattcgc tacgagggag 300
tttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagtttta agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390, and 396 are either A, T, G, or C.

<400> 7
nagaaaaaaag tgaacaaaat gtttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60
ggagctttc cctgcacaag gntcccgccgc antcgccag cccgtccaga actgcagcca 120
cccccccccgn tttcctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180
tctggacttc tcgggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

ggcggtcatc tatccgcttc agtcctcggtt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat cttcccaac catgggggg aggagcttgg ggcactngtt ttcaaaaatt 360
gggggatcag gggacaaaact ttgattggan cccatnttgg ggcttttggg cctttgggc 420
aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203,
206, 238, 252, 297, 370, 389, and 427 are either
A, T, G, or C.

<400> 8
ttttttttt tttttttgt atcagtgaac aaaatggttc ttagaaaaca tggtcttgt 60
gttnccagggtg cccagggagc tcttccotgc acaagganc cgcgcantcg gccagccgt 120
ccagaactgc agccacgccc cccgtttcc tcagggcacag tctccttcac tgttttcac 180
atctctgnntt ctctctctgg ganttnctgg tgggccccag aacgtcaagc tgtcagtntt 240
cttctgttaac tnttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgtatntt 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatgggg gaaggagttt 360
gggtcaattn tttcaaaac attggggntt cagggacaaa atttgtatgg aaacccaatt 420
tgggggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttt actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc acgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagttt 240
tcctgatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA

<213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcggt ggtggactgt 120
ttactggaag aatattttat gcagagtgc acgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgc 240
tgtccaatgt 250

<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 155, 393, and 442 are either A, T, G, or C.

<400> 11

gattaatcttg gccactgaca tggcaagaca tgcagaaatt atggatttt tcaaagagaa 60
aaatggagaat tttgactaca gcaacgagga gcacatgacc ctggtagtg gcttattctg 120
cctgggtgg cagccaggcg gttggctgg cgaanagggtt catccatcca gtcacactg 180
gaagccaaaga agctgaaatt attagtcttc ttggacaag gtgtctataa atctggttt 240
caaggtcatg actcttacta ggaaagtccg ggcaggccct ccctcctgat gggcctcct 300
tcatggtcag aggacgcatt ctccattcc tccatctctt ttgggattt gaaggagata 360
aagtgggtg aaggccgtgc attctcgctc tgnntttcca gagaattaaa accagtttc 420
ccttgaaggc acagccccag cttggcattt tgaaagttg 459

<210> 12

<211> 599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99)..(443)

<400> 12

tggccctcga ggccaagaat tcggcacgag tggtaactg ggcacatctt tctttctctg 60

agaacagcga tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116

Cys His Cys Leu Leu His

1

5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro	10	15	20	164	
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe	25	30	35	212	
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe	40	45	50	260	
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp	55	60	65	70	308
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln	75	80	85	356	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu	90	95	100	404	
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgagggaaagc Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala	105	110	115	453	
ggggggcggtg gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtcaggg aagagctgcc ctggcacct ggcaccacaa gaccatgttt tctaagaacc atttgttca				513	
ctgataaaaa aaaaaaaaaa aaaaaa <210> 13 <211> 115 <212> PRT <213> Homo sapiens				573	
<400> 13 Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu 1 5 10 15					
Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala 20 25 30					
Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu 35 40 45					
Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro 50 55 60					
Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp 65 70 75 80					
Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala					

85

90

95

Thr Glu Lys Ser Arg Glu Arg Ser Asp Val Lys Asn Ser Glu Gly
100 105 110

Asp Cys Ala
115

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
agtgcattt accgtgagaa gtcagaag 28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtcaaaggctt acatggcttt gtggtgcc 28

<210> 16
<211> 1303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)..(1066)

<400> 16
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cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115
Ala Leu Glu
1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
20 25 30 35

aac ccc ttc cac aac ttc cg ^g cac tgc ttc tgc gt ^g gcc cag at ^g at ^g	259
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met	
40 45 50	
tac agc at ^g gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa ac ^g	307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr	
55 60 65	
gat at ^c ctg at ^c cta at ^g aca gc ^g gcc at ^c tgc cac gat ctg gac cat	355
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His	
70 75 80	
ccc ggc tac aac aac ac ^g tac cag at ^c aat gcc cg ^c aca gag ctg gc ^g	403
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala	
85 90 95	
gtc cg ^c tac aat gac at ^c tca cc ^g ctg gag aac cac cac tgc gcc gt ^g	451
Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val	
100 105 110 115	
gcc ttc cag at ^c ctc gc ^c gag cct gag tgc aac at ^c ttc tcc aac at ^c	499
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile	
120 125 130	
cca cct gat ggg ttc aag cag at ^c cga cag gga at ^g at ^c aca tta at ^c	547
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile	
135 140 145	
ttg gcc act gac at ^c gca aga cat gca gaa att at ^c gat tct ttc aaa	595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys	
150 155 160	
gag aaa at ^c gag aat ttt gac tac agc aac gag gag cac at ^c acc ct ^g	643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu	
165 170 175	
ctg aag at ^c att ttg ata aaa tgc tgt gat at ^c tct aac gag gtc cgt	691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg	
180 185 190 195	
cca at ^c gaa gtc gca gag cct tgg gt ^g gac tgt tta tta gag gaa tat	739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr	
200 205 210	
ttt at ^c cag agc gac cgt gag aag tca gaa ggc ctt cct gt ^g gca cc ^g	787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro	
215 220 225	
ttc at ^c gac cga gac aaa gt ^g acc aag gcc aca gcc cag att ggg ttc	835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe	
230 235 240	
at ^c aag ttt gtc ctg at ^c cca at ^c ttt gaa aca gt ^g acc aag ctc ttc	883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe	
245 250 255	
ccc at ^c gtt gag gag at ^c at ^c ctg cag cca ctt tgg gaa tcc cga gat	931

Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp				
260	265	270	275	
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag				979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln				
280	285	290		
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag				1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu				
295	300	305		
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc				1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala				
310	315	320		
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aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca				1196
ctgatacacaa aaaaaaaaaaag gaattcatga tgctgtacag aattttatTT taaaactgtc				1256
ttttaataaa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaaaaa				1303
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Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser				
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Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn				
20	25	30		
Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala				
35	40	45		
Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe				
50	55	60		
Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp				
65	70	75	80	
Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr				
85	90	95		
Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His				
100	105	110		
Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe				
115	120	125		
Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile				
130	135	140		

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160
 Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175
 Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190
 Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205
 Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220
 Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 225 230 235 240
 Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
 245 250 255
 Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
 260 265 270
 Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
 275 280 285
 Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
 290 295 300
 Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 305 310 315 320

<210> 18
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 <212> DNA
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<220>
 <221> CDS
 <222> (74)..(1672)

<400> 18
 ctcccccggcc tccccggcg gctggcgctcg ggaaagtaca gtaaaaagtc cgagtgcagc 60
 cggccgggccc agg atg gga tcc ggc tcc agc tac cgg ccc aag gcc 109
 Met Gly Ser Gly Ser Ser Tyr Arg Pro Lys Ala
 1 5 10

atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
 Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
 15 20 25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
 Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
 30 35 40

ctg cct cg ^a aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met	45 50 55 60	253
gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr	65 70 75	301
aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu	80 85 90	349
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	95 100 105	397
aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	110 115 120	445
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	125 130 135 140	493
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	145 150 155	541
agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	160 165 170	589
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	175 180 185	637
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	190 195 200	685
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	205 210 215 220	733
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	225 230 235	781
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	240 245 250	829
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	255 260 265	877
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc		925

Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile			
270	275	280	
ctc atg aca gca gcc atc tgc cac gat ctg gac cat ccc ggc tac aac			973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn			
285	290	295	300
aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat			1021
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn			
305	310	315	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ctc cag atc			1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile			
320	325	330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg			1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly			
335	340	345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac			1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp			
350	355	360	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag			1213
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu			
365	370	375	380
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att			1261
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile			
385	390	395	
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc			1309
Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val			
400	405	410	
gca gag cct tgg gtc gac tgt tta tta gag gaa tat ttt atg cag agc			1357
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser			
415	420	425	
gac cgt gag aag tca gaa ggc ctt cct gtc gca ccg ttc atg gac cga			1405
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
430	435	440	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc			1453
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
445	450	455	460
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag			1501
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
465	470	475	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag			1549
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
480	485	490	
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac			1597
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp			

495

500

505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 1645
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
 510 515 520

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1692
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 525 530

gctgcagttc tggacgggct ggccgagctg cgcggatcc ttgtcaggg aagagctgcc 1752
 ctggcacct ggcaccacaa gaccatgttt tctaagaacc attttggcca ctgataaaaa 1812
 aaaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt ctttaaata 1872
 atatattctt atacg 1887

<210> 19
<211> 533
<212> PRT
<213> Homo sapiens

<400> 19
Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
 1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205
 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255
 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270
 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285
 Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300
 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
 305 310 315 320
 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
 325 330 335
 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
 340 345 350
 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415
 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
 420 425 430
 Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
 435 440 445
 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
 450 455 460
 Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
 465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
485 490 495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
500 505 510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
515 520 525

Glu Gly Asp Cys Ala
530

<210> 20

<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1741)

<400> 20

c tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag tac 49
Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
1 5 10 15

tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu

130

135

140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu 145 150 155 160	481
aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu 165 170 175	529
ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile 180 185 190	577
aag aag atg agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195 200 205	625
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220	673
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240	721
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255	769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270	817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285	865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300	913
ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305 310 315 320	961
cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gca gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335	1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340 345 350	1057
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365	1105

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag		1153
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu		
370	375	380
tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga		1201
Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg		
385	390	395
395	400	
cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca		1249
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala		
405	410	415
gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc		1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser		
420	425	430
aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt		1345
Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys		
435	440	445
gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg		1393
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val		
450	455	460
gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca		1441
Asp Cys Leu Leu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser		
465	470	475
475	480	
gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag		1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys		
485	490	495
gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt		1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe		
500	505	510
gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag		1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln		
515	520	525
cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat		1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp		
530	535	540
gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg		1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly		
545	550	555
555	560	
gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa		1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu		
565	570	575
gga gac tgt gcc tgaggaaaagc gggggcgctg gctgcagtcc tggacgggct		1781
Gly Asp Cys Ala		
580		
ggccgagctg cgccggatcc ttgtgcaggg aagagctgcc ctggcacct ggcaccacaa		1841

gaccatgttt tctaagaacc attttggta ctgatacaaa aaaaaaaaaa ggaattcatg 1901
atgctgtaca gaattttatt tttaactgt cttttaata atatattctt atacggaaaa 1961
aaaaaaaaa 1967

<210> 21
<211> 580
<212> PRT
<213> Homo sapiens

<400> 21
Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
1 5 10 15

Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
245 250 255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
260 265 270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
275 280 285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
435 440 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
450 455 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
530 535 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545 550 555 560

Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
565 570 575

Gly Asp Cys Ala
580

<210> 22
<211> 1457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (164)..(1453)

<400> 22
ggctccggg cgtcccgcc ccgggtggcgg cgccggctgtg gttggctgag cgccgcggc 60
cgccccccgc ccgccccctc ccctgctccc ctccccccgc tcccgccggc gctggcgtcg 120
ggaaagtaca gtaaaaagtc cgagtgcage cgccgggcgc agg atg gga tcc ggc 175
Met Gly Ser Gly
1
tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
5 10 15 20
att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
25 30 35
gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
40 45 50
ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
55 60 65
gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
70 75 80
caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463 /
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
85 90 95 100
gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
105 110 115
gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga 559

345	350	355	
atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met 360	365	370	1279
gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu 375	380	385	1327
cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser 390	395	400	1375
aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu 405	410	415	1423
tta gag gaa tat ttt atg cag agc gac cgt gaga Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg 425	430		1457
<210> 23			
<211> 430			
<212> PRT			
<213> Homo sapiens			
<400> 23			
Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp 1 5 10 15			
Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser 20 25 30			
Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn 35 40 45			
Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50 55 60			
Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro 65 70 75 80			
Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val 85 90 95			
Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 100 105 110			
Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115 120 125			
Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 130 135 140			
Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn			

145	150	155	160
Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro			
165		170	175
Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr			
180		185	190
Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro			
195	200		205
Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu			
210	215		220
Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe			
225	230		235
Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His			
245		250	255
Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser			
260		265	270
Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala			
275	280		285
Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln			
290	295		300
Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro			
305	310		315
Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro			
325		330	335
Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile			
340		345	350
Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His			
355		360	365
Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr			
370	375		380
Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys			
385	390		395
Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp			
405		410	415
Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg			
420		425	430

<210> 24
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 24

Asp Thr Lys Asp Asp Asp Lys
1 5

<210> 25

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact

54

<210> 26

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26

cgaggaggta acttcttg

18